Amendments to the Claims

Claim 1 (Currently Amended). A method for the directed integration of an expressible DNA fragment lacking a selectable marker into a bacterial chromosome of an *E. coli* comprising:

a) providing at least one first recombination element having the general structure in the 5' to 3' direction:

5'-RR1-RS-SM-RS-RR2-3'; wherein

(i) RR1 is a first recombination region of about 10 to 50 bases;

(ii) RS is a recombination site responsive to a site-specific recombinase;

(iii) SM is a DNA fragment encoding a selectable marker; and

(iv) RR2 is a second recombination region of about 10 to 50 bases;

b) providing at least one second recombination element having the general structure in a 5' to 3' direction:

X-RR3; wherein

(i) X is an expressible DNA fragment having homology to the second recombination ~~region~~element; and

(ii) RR3 is a third recombination region of about 10-50 bases,

c) providing a recombination proficient bacterial host harboring a λ-Red recombinase system, having a bacterial chromosome comprising:

(i) a first chromosomal region having homology to said first recombination region and wherein said first chromosomal region is either upstream of a bacterial promoter or an inter-operon chromosomal integration site;

(ii) a second chromosomal region having homology to said third recombination region;

d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction;

5'-RR1-RS-SM-RS-RR2-X-RR3;

e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;

f) expressing a site-specific recombinase in the isolated hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the expressible DNA fragment is inserted into the bacterial chromosome, lacking the selectable marker.

Claim 2 (Canceled)

Claim 3 (Previously Presented). A method according to Claim 1 wherein either the first expressible DNA fragment is selected from the group consisting of regulatory elements, promoters, genes, coding sequences, and open reading frames.

Claim 4 (Previously Presented). A method according to Claim 1 wherein the site-specific recombinase is expressed by a gene residing on a plasmid.

Claim 5-6 (Canceled).

Claim 7 (Original). A method according to Claim 3 wherein said expressible DNA fragment is a promoter selected from the group consisting of bacterial and phage promoters.

Claim 8 (Original). A method according to Claim 7 wherein said promoter comprises positive and negative regulatory sites for control of a regulatory circuit.

Claim 9 (Previously Presented). A method according to Claim 8 wherein said regulatory circuit comprises a *lac* operator site.

Claim 10 (Previously Presented). A method according to Claim 7 wherein said promoter is selected from the group consisting of a phage *T5* promoter, a phage *T7* promoter, and a *lac* promoter.

Claim 11 (Previously Presented). A method according to Claim 1 wherein said selectable marker is selected from the group consisting of antibiotic resistance markers, enzymatic markers and amino acid biosynthesis enzymes.

Claim 12 (Canceled).

Claim 13 (Previously Presented). A method according to Claim 1wherein said recombination sites are selected from the group consisting of *lox*, *frt*, *dif*, and *att*.

Claim 14 (Original). A method according to Claim 13 wherein said site-specific recombinase is selected from the group consisting of Cre, Flp, Xer, and Int.

Claim 15 (Previously Presented). A method according to Claim 1wherein said recombination elements are generated by PCR.

Claim 16 (Previously Presented). A method according to Claim 1 wherein said recombination elements are from about 25 bases to about 4000 bases.

Claim 17 (Currently Amended). A method for the integration of a foreign promoter in place of a bacterial chromosomal promoter in a recombination proficient *E. coli* host cell comprising:

a) providing at least one first recombination element having the general structure in the 5' to 3' direction:

5'-RR1-RS-SM-RS-RR2-3'; wherein

(i) RR1 is a first recombination region of about 10 to 50 bases;

(ii) RS is a recombination site responsive to a site-specific recombinase;

(iii) SM is a DNA fragment encoding a selectable marker; and

(iv) RR2 is a second recombination region of about 10 to 50 bases;

b) providing at least one second recombination element having the general structure in a 5' to 3' direction:

5'-FP-RR3-3'; wherein

(i) FP is a promoter foreign to the recombination proficient host cell having homology to the second recombination region wherein said promoter is selected from the group consisting of a phage *T5* promoter, a phage *T7* promoter, and a *lac* promoter; and

(ii) RR3 is a third recombination region of about 10-50 bases,

c) providing a recombination proficient bacterial host harboring a λ-Red recombinase system, having a bacterial chromosome comprising:

(i) a first chromosomal region upstream of a bacterial promoter having homology to said first recombination region;

(ii) a second chromosomal region, downstream of said bacterial promoter having homology to said third recombination region;

d) transforming said recombination proficient host with the first and second recombination elements, wherein both elements are integrated into the bacterial chromosome between the first and second chromosomal regions forming a construct having the general structure in the 5' to 3' direction;

5'-RR1-RS-SM-RS-RR2-FP-RR3;

e) selecting and isolating transformed hosts having the construct of (d) on the basis of the selectable marker;

f) expressing a site-specific recombinase in the isolated hosts of (e) wherein the selectable marker is excised from the chromosome and whereby the foreign promoter is inserted into the bacterial chromosome in place of the bacterial promoter.

Claims 18 – 19 (Canceled)

Claim 20 (Previously Presented). A method according to Claim 17 wherein the site-specific recombinase is expressed by a gene residing on a plasmid.

Claim 21-25 (Canceled).

Claim 26 (Previously Presented). A method according to Claim 17 wherein said recombination sites are selected from the group consisting of *lox*, *frt, dif,* and *att*.

Claim 27 (Original). A method according to Claim 26 wherein said site-specific recombinase is selected from the group consisting of Cre, Flp, Xer, and Int.

Claim 28 (Previously Presented). A method according to Claim 17 wherein said recombination elements are generated by PCR.

Claim 29 (Previously Presented). A method according to Claim 17 wherein said recombination elements are from about 25 bases to about 4000 bases.

Claim 30 (Currently Amended). A method according to any of Claims 31, or 17

wherein steps (d) – (f) are repeated one or more times.